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WHAT IS CLAIMED IS:

1. A method for predicting resistance of a pathogen to a therapeutic agent comprising:
- (a) providing a trained neural network;
 - (b) providing a determined genetic sequence from the pathogen; and
 - (c) predicting resistance of the pathogen to the therapeutic agent using the determined genetic sequence and the trained neural network.
2. The method of claim 1, wherein the pathogen is chosen from a disease-producing bacterium, a disease-producing virus, a disease-producing algae, a disease-producing fungus and a disease-producing protozoa.
3. The method of claim 2, wherein the pathogen is a disease-producing virus.
4. The method of claim 3, wherein the disease-producing virus is chosen from human immunodeficiency virus type 1, human immunodeficiency virus type 2, herpes simplex virus type 1, herpes simplex virus type 2, human papillomavirus virus, hepatitis B virus, hepatitis C virus, and Epstein-Barr virus.
5. The method of claim 4, wherein the disease-producing virus is the human immunodeficiency virus type 1.
6. The method of claim 1, wherein the trained neural network is a three-layer feed-forward neural network.
7. The method of claim 6, wherein the three-layer feed forward network comprises:
- (a) a set of input nodes, wherein each member of the set of input nodes corresponds to a mutation in the genome of the pathogen;
 - (b) a plurality of hidden nodes; and
 - (c) a set of output nodes, wherein each member of the set of output nodes corresponds to a therapeutic agent used to treat the pathogen.
8. A method for predicting resistance of a disease to a therapeutic agent comprising:
- (a) providing a trained neural network;
 - (b) providing a determined genetic sequence from the disease; and
 - (c) predicting resistance of the disease to the therapeutic agent using the determined genetic sequence and the trained neural network.

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27. The method of claim 26, wherein the disease-producing virus is chosen from human immunodeficiency virus type 1, human immunodeficiency virus type 2, herpes simplex virus type 1, herpes simplex virus type 2, human papillomavirus virus, hepatitis B virus, hepatitis C virus, and Epstein-Barr virus.

5 28. The method of claim 27, wherein the disease-producing virus is the human immunodeficiency virus type 1.

29. A method of predicting the probability of a patient developing a genetic disease comprising:

- (a) providing a trained neural network;
- 10 (b) providing a determined genetic sequence from a patient sample; and
- (c) determining the probability of the patient of developing the genetic disease using the determined genetic sequence and the trained neural network.

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